

FIG. 1A

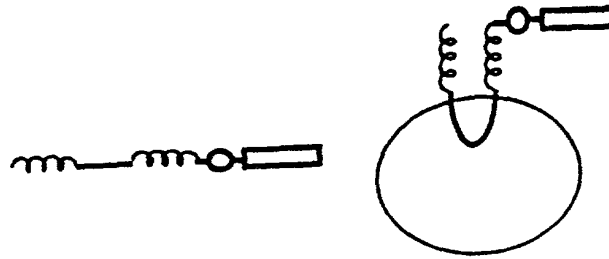


FIG. 1B

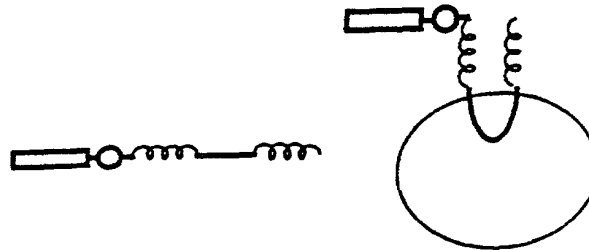


FIG. 1C

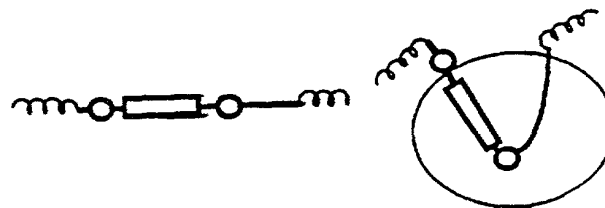
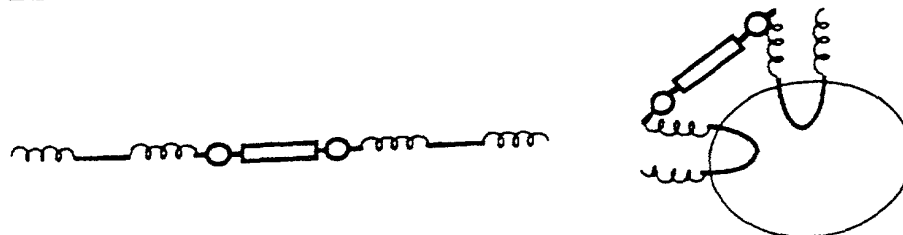


FIG. 1D



-667 ^{NcoI}
 CCATGCGCTATACCCAACTCGGTCTTGGTCACACCGAAGCTCTCTGGTAAGCTAGCTCCACTCCCCAGAAACAACCGGCCCAAAATTGC
 -777 CGGAATTGCTGACCTGAAGACGGAACATCATCGTCGGGTCTCTGGGCGATTCGGCGCGGAAGATGGGTACAGCTTGGGCTTGAGGACGAGAC
 -687 CGGAATCGAGTCTGTTGAAAGGTTGTTTCATTGGGATTTGTATACGGAGATTTGGTCTGCGAGAGCTTTGAGGGAAAGSACAAATGGGTTTTG
 R1
 -597 GCTCTCGAGAAAGAGAGTGGCGCTTTTAGAGAGAGAAATTGAGAGCTTTTAGAGAGAGATGCGGCGCGGATGACGGGAGGAGAGACGACGAGG
 R2 R2
 -507 ACCTGCATTATCAAAGCAGTGACGTGGTGAAATTTGGAACCTTTTAGAGGCGAGATAGATTTATTATTGTATCCATTTTCTTCATTGTTT
 R1
 -417 TAGAATGTCGCGGAACAAATTTTAAACTAAATCCTAAATTTTCTTAATTTTGTTCGCAATAGTGGATATGTGGCCGTATAGAAGGAAT
 -327 CTATTGAAGGCCCAACCCATCTAGACGAGCCCAAGGTTTCGTTTTGCGTTTTATGTTTTGCGTTTCGATGCCAACGCCACATTCCTGAGCTA
 I
 -237 GGCAAAAACAAACGTTGCTTTGAATAGACTCCTCTCGTTAACACATGCGAGCGGCTGCATGGTGACGCCATTAACACGCTGGCTACAAT
 -147 GCATGATGTCCTCATTTGACACGTGACTTCTCGTCTCCTTTCTTAATATATCTAAACAACTCTTACCTCTTCCAAAAATATATACACATC
 M A D T A R G T H H D
 57 TTTTGTGATCAATCTCTCATTCAAATCTCATTCTCTCTAGTAAACAAGAACAAAAAATGCGGATACAGCTAGAGGAACCCATCAGGAT
 I I G R D O Y P M M G R D R D O Y Q M S G R G S D Y S K S R
 34 ATCATCGGCAGAGACCACTACCCGATGATGGGCCGAGACCGAGACCACTACAGATGTCGCGACGAGGATCTGACTACTCCAACTCAGG
 O I A K A A T A V T A G G S L L L V L S S L T L V G T V I A L
 124 CAGATTGCTAAAGCTGCACTGCTGCACAGCTGGTGGTCCCTCTCTGTTCTCCAGCCTTACCCTTGTTGGAATGTGCATAGCTTTG
 T V A T P L L V I F S P I L V P A L I T V A L L I T G F L S
 214 ACTTGTGCACACCTCTGCTCGTTATCTTCAGCCCAATCCTGTGCCCGCTCTCATCAGCTTCACCTCCTCATACCGGTTTCTTTCC
 S G C F G I A A I T V F S W I Y K
 304 TCTGGAGGGTTTGGCATTGGCGCTATAACCGTTTTCTCTGGATTTACAAGtaagcacacatttatcatcttacttcataattttgtgca
 394 atatgtgcatgcatgtgttgagccagtagcttttggatcaatttttttgggtcgaataacaatgtaacaataagaatttgc aaatttctagg
 484 gaacatttgggttaactaaatacgaattttagcctagcttagcttgaatgtgtctgtgtatatcatctatataggtaaaaatgcttggtatga
 Y A T G G E H P Q G S D K L D S A R M K L G S K
 574 taectattgattgtgtaatagGTACGCAACGGGAGAGACCCACAGGATCAGACAAGTTGGACAGTGCACAGGATGAAGTTGGGAAGCAAA
 A O D L K D R A Q Y Y G Q Q H T G G E H D R D R T R G G Q H
 664 GCTCAGGATCTGAAAGACAGAGCTCAGTACTACGGACAGCAACATACTGGTGGGAACATGACCGTGACCGTACTCGTGGTGGCCAGCAC
 T T *
 754 ACTACTTAAGTTACCCCACTGATGTGCATCGTCATAGTCCAATAACTCCAATGTGCGGGAGTTAGTTTTATGAGGAATAAAGTGTTTAGAAT
 Kpnl
 844 TTGATCAGGGGGAGATAATAAAGCCGAGTTTGAATCTTTTGTGTATAAGTAATGTTTATGTGTGTTTCTATATGTTGTCAAAATGGTACC

FIGURE 3

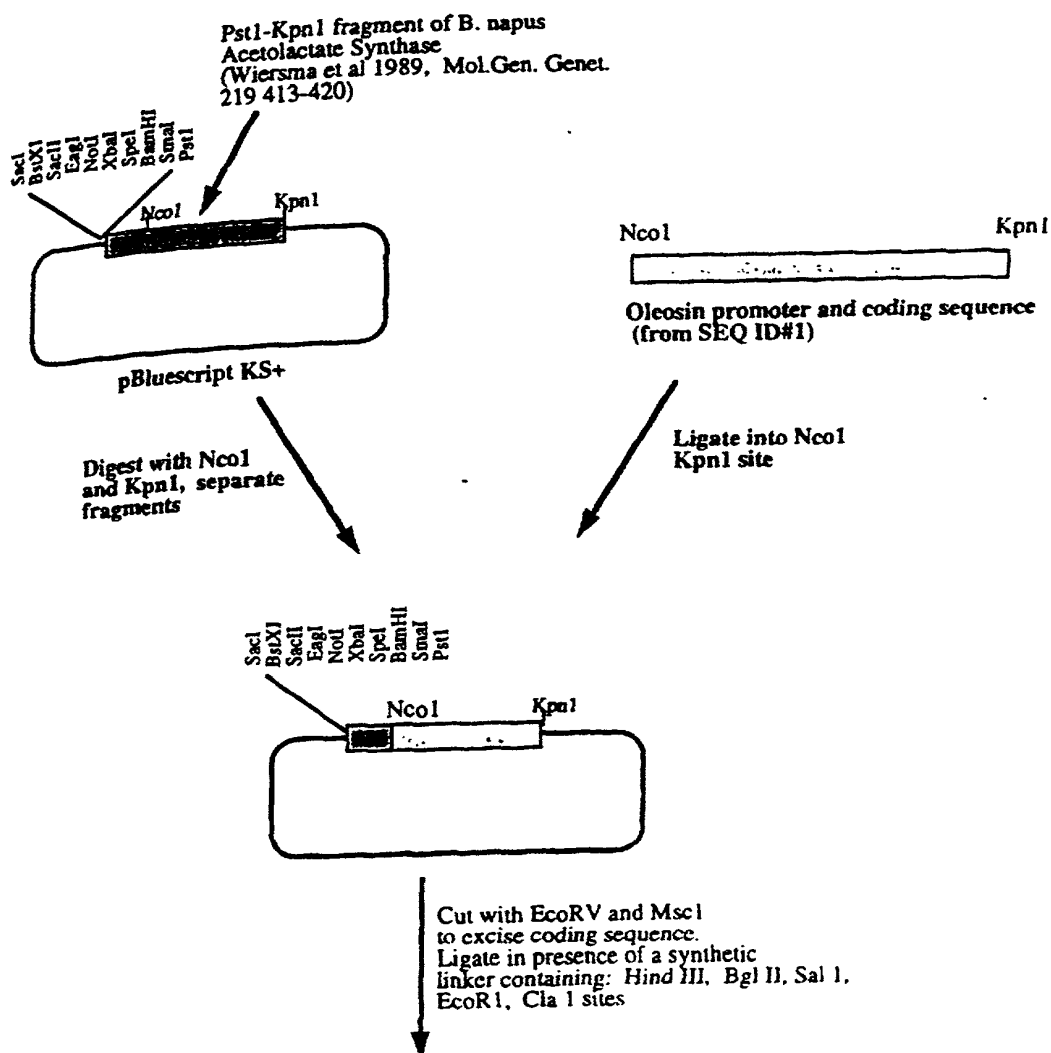


FIG 3

FIGURE 3 cont'd

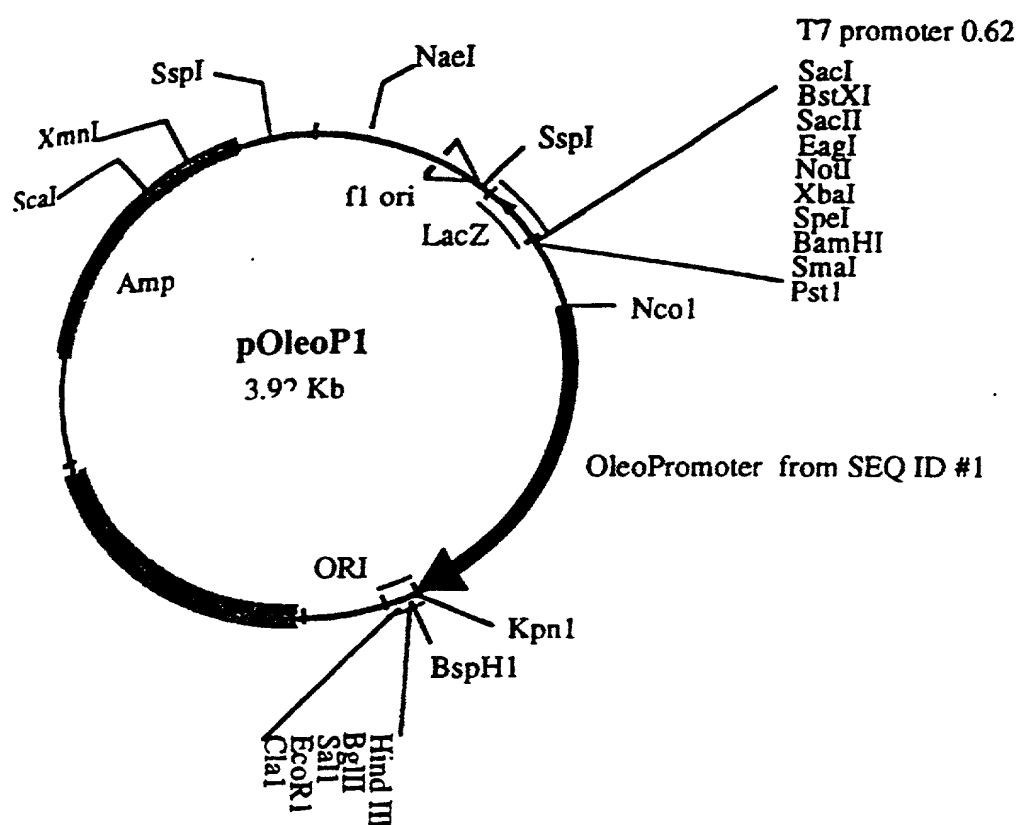


FIGURE 4

1 ATG GCG GAT ACA GCT AGA ACC CAT CAC GAT GTC ACA AGT CGA GAT CAG TAT CCC CGA GAC 60
1 M A D T A R T H H D V T S R D Q Y P R D 20

61 CGA GAC CAG TAT TCT ATG ATC GGT CGA GAC CGT GAC CAG TAC TCT ATG ATG GGC CGA GAC 120
21 R D Q Y S M I G R D R D Q Y S M M G R D 40

121 CGA GAC CAG TAC AAC ATG TAT GGT CGA GAC TAC TCC AAG TCT AGA CAG ATT GCT AAG GCT 180
41 R D Q Y N M Y G R D Y S K S R Q I A K A 60

181 GTT ACC GCA GTC ACG GCG GGT GGG TCC CTC CTT GTC CTC TCC AGT CTC ACC CTT GTT GGT 240
61 V T A V T A G G S L L V L S S L T L V G 80

241 ACT GTC ATT GCT TTG ACT GTT GCC ACT CCA CTC CTC GTT ATC TTT AGC CCA ATC CTC GTG 300
81 T V I A L T V A T P L L V I F S P I L V 100

301 CCG GCT CTC ATC ACC GTA GCA CTT CTC ATC ACT GGC TTT CTC TCC TCT GGT GGG TTT GCC 360
101 P A L I T V A L L I T G F L S S G G F A 120

361 ATT GCA GCT ATA ACC GTC TTC TCC TGG ATC TAT AAG TAC GCA ACG GGA GAG CAC CCA CAG 420
121 I A A I T V F S W I Y K Y A T G E H P Q 140

421 CCG TCA GAT AAG TTG GAC AGT GCA AGG ATG AAG CTG GGA ACC AAA GCT CAG GAT ATT AAA 480
141 G S D K L D S A R M K L G T K A Q D I K 160

481 GAC AGA GCT CAA TAC TAC GGA CAG CAA CAT ACA GGT GGT GAG CAT GAC CGT GAC CGT ACT 540
161 D R A Q Y Y G Q Q H T G G E H D R D R T 180

541 CGT GGT GGC CAG CAC ACT ACT TAA 564
181 R G G Q H T T *

0000425-07004

FIGURE 5

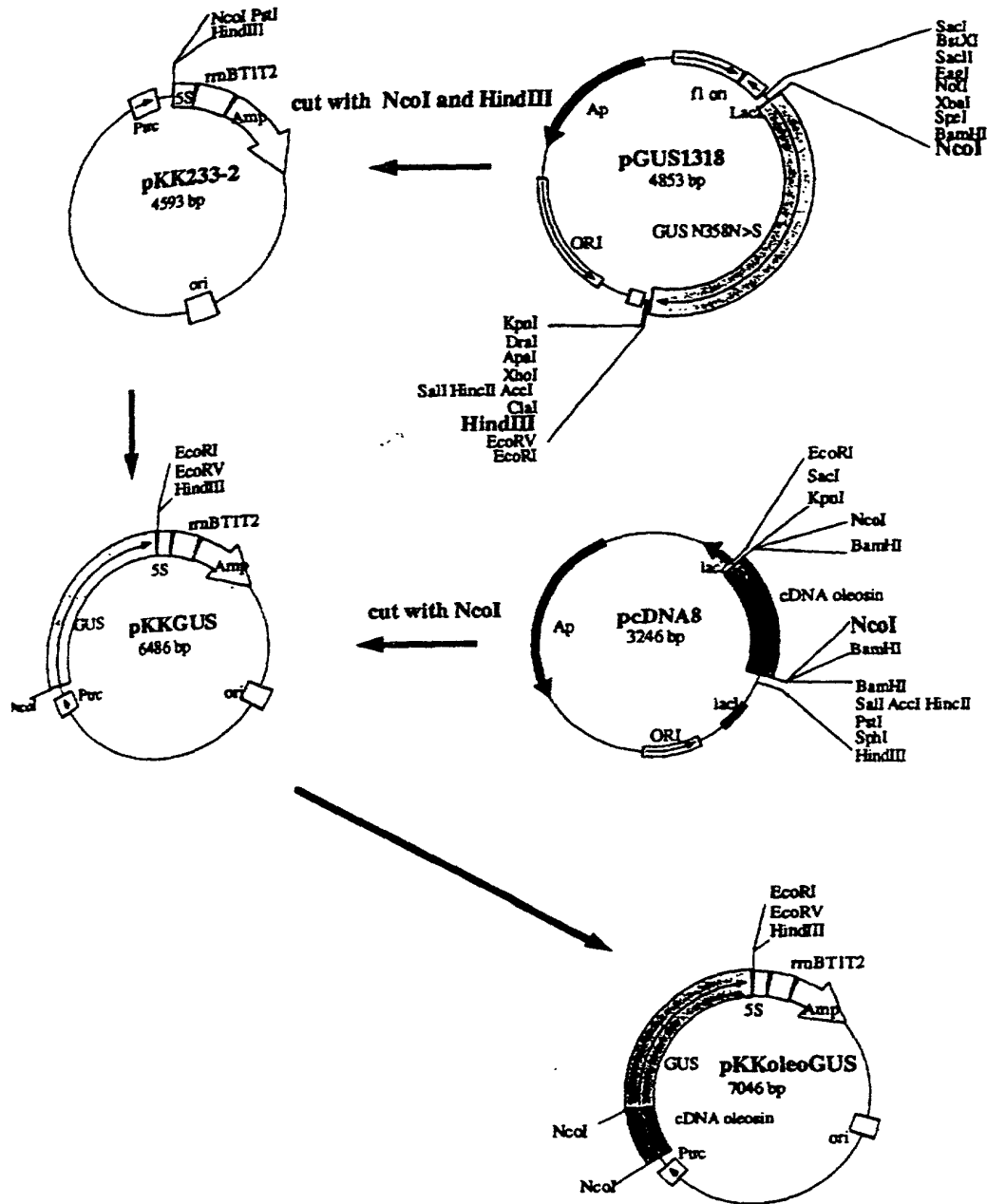


FIGURE 6

HindIII

1	ATAAGCTTGCATGCCTGCGGAACCTCTCTGGTAAGCTAGCTCCACTCCCCAGAAACAACCG	60
61	GCGCCAAATTGCCGGAATTGCTGACCTGAAGACGGAACATCATCGTCGGGTCCTTGGGCG	120
121	ATTGCGGCGGAAGATGGGTTCAGCTTGGGCTTGAGGACGAGACCCGAATCGAGTCTGTTGA	180
181	AAGGTGTGTTTCATTGGGATTGTATACGGAGATTGGTTCGTCGAGAGGTTTGAGGGAAAGGA	240
241	CAAAATGGGTTTGGCTCTGGAGAAAGAGAGTGGGCTTTAGAGAGAGAATTGAGAGGTTTA	300
301	GAGAGAGATCGGCGGCGATGACGGGAGGAGAGACGACGAGGACCTGCATTATCAAAGCA	360
361	GTGACGTGGTGAAATTTGGAACCTTTTAAGAGGCAGATAGATTTATTATTTGTATCCATT	420
421	TCTTCATTGTTCTAGAATGTGCGGGAACAAATTTTAAACTAAATCCTAAATTTTCTAA	480
481	TTTTGTTGCCAATAGTGGATATGTGGGCCGTATAGAAGGAATCTATTGAAGGCCCAACC	540
541	CATACTGACGAGCCCAAAGGTTTCGTTTTCGTTTATGTTTCGTTTCGATGCCAACGCCA	600
601	CATTCTGAGCTAGGCAAAAAACAAACGTGTCTTTGAATAGACTCCTCTCGTTAACACATG	660
661	CAGCGGCTGCATGGTGACGCCATTAACACGTGGCTACAATTGCATGATGTCTCCATTGA	720
721	CACGTGACTTCTCGTCTCCTTTCTTAATATATCTAACAAACACTCCTACCTCTTCCAAA	780
781	TATATACACATCTTTTGATCAATCTCTCATTCAAATCTCATTCTCTCTAGTAACAAG	840
	M A D T A R G T H H D I I G R D Q	
841	AACAAAAAATGGCGGATACAGCTAGAGGAACCCATCAGGATATCATCGGACAGAGACCAG	900
	Y P M M G R D R D Q Y Q M S G R G S D Y	
901	TACCCGATGATGGGCGAGACCGAGACCAGTACCAGATGTCCGGACGAGGATCTGACTAC	960
	S K S R Q I A K A A T A V T A G G S L L	
961	TCCAACTCTAGGCAGATTGCTAAAGCTGCAACTGCTGTCTACAGCTGGTGGTTCCCTCCTT	1020
	V L S S L T L V G T V I A L T V A T P L	
1021	GTTCTCTCCAGCCTTACCCTTGTGGAACTGTCTAGCTTTGACTGTTGCAACACCTCTG	1080
	L V I F S P I L V P A L I T V A L L I T	
1081	CTCGTTATCTTCAGCCCAATCCTTGTCCCGGCTCTCATCACAGTTGCACTCCTCATACC	1140
	G F L S S G G F G I A A I T V F S W I Y	
1141	GGTTTTCTTCTCTGGAGGGTTTGGCATTGCCGCTATAACCGTTTTCTCTTGGATTAC	1200
	K	
1201	AAGTAAGCACACATTTATCATCTTACTTCATAATTTTGTGCAATATGTGCATGCATGTGT	1260
1261	TGAGCCAGTAGCTTTGGATCAATTTTGTGGTGAATAACAAATGTAACAATAAGAAATT	1320
1321	GCAAATCTAGGGAACATTTGGTTAACTAAATACGAAATTTGACCTAGCTAGCTTGAATG	1380
1381	TGTCTGTGTATATCATCTATATAGGTAAATGCTTGGTATGATACCTATTGATTGTGAAT	1440
	Y A T G E H P Q G S D K L D S A R M K	
1441	AGTACGCAACGGGAGAGACCCACAGGGATCAGACAAGTTGGACAGTGCAAGGATGAAG	1500
	L G S K A Q D L K D R A Q Y Y G Q Q H T	
1501	TTGGGAAGCAAAGCTCAGGATCTGAAAGACAGAGCTCAGTACTACGGACAGCAACATACT	1560
	G G E H D R D R T R G G Q H T T L V P R	
1561	GGTGGGGAACATGACCGTGACCGTACTCGTGGTGGCCAGCACACTACTCTCGTTCCACGA	1620
	G S M A E I T R I P L Y K G K S L R K A	
1621	GGATCCATGGCTGAGATCACCAGGATCCCTCTGTACAAAGGCAAGTCTCTGAGGAAGCGG	1680
	L K E H G L L E D F L Q K Q Q Y G I S S	
1681	CTGAAGGAGCATGGGCTTCTGGAGGACTTCTGCGAGAAACAGCAGTATGGCATCAGCAGC	1740
	K Y S G F G E V A S V P L T N Y L D S Q	
1741	AAGTACTCCGGCTTCGGGGAGGTGGCCAGCGTGCCCTGACCAACTACCTGGATAGTCAG	1800

	Y F G K I Y L G T P P Q E F T V L F D T	
1801	TACTTTGGGAAGATCTACCTCGGGACCCCCGCCCCAGGAGTTCCACGCTGCTGTTTGACACT G S S D F W V P S I Y C K S N A C K N H	1860
1861	GGCTCCTCTGACTTCTGGGTACCCTCTATCTACTGCAAGAGCAATGCCTGCAAAAACAC Q R F D P R K S S T F Q N L G K P L S I	1920
1921	CAGCGCTTCGACCCGAGAAAGTCGTCCACITCCAGAACCTGGGCAAGCCCCTGTCTATC H Y G T G S M Q G I L G Y D T V T V S N	1980
1981	CACTACGGGACAGGCAGCATCGAGGGCATCCTGGGCTATGACACCTGTCTACTGTCTCCAAC I V D I Q Q T V G L S T Q E P G D V F T	2040
2041	ATTGTGGACATCCAGCAGACAGTAGGCCCTGAGCACCCAGGAGCCCCGGGACGTCTTCACC Y A E F D G I L G M A Y P S L A S E Y S	2100
2101	TATGCCGAATTCGACGGGATCCTGGGGATGGCCTACCCCTCGCTCGCCTCAGAGTACTCG I P V F D N M M N R H L V A Q D L F S V	2160
2161	ATACCCGTGTTTGACAACATGATGAACAGGCACCTGGTGGCCCAAGACCTGTTCTCGGTT Y M D R N G Q E S M L T L G A I D P S Y	2220
2221	TACATGGACAGGAATGGCCAGGAGSACATGCTACGCTGGGGGCCATCGACCCGTCCTAC Y T G S L H W V P V T V Q Q Y W Q F T V	2280
2281	TACACAGGTCCTCGCACTGGGTGCCCCGTGACAGTGCAGCAGTACTGGCAGTTCACTGTG D S V T I S G V V V A C E G G C Q A I L	2340
2341	GACAGTGCACCATCAGCGGTGTGGTTGTGGCCTGTGAGGGTGGCTGTGAGGCCATCTTG D T G T S K L V G P S S D I L N I Q Q A	2400
2401	GACACGGGCACCTCCAAGCTGGTCGGGCCCCAGCAGCGACATCCTCAACATCCAGCAGGCC I G A T C Q N Q Y G E F D I D C D N L S Y	2460
2461	ATTGGAGCCACAGAACAGTACGGTGAGTTTGACATCGAGTCGGACAACCTGAGCTAC M P T V V F E I N G K M Y P L T P S A Y	2520
2521	ATGCCCCACTGTGGTCTTTGAGATCAATGGCAAAATGTACCCACTGACCCCCCTCCGCCTAT T S Q D Q G F C T S G F Q S E N H S Q K	2580
2581	ACCAGCCAAGACCAGGGCTTCTGTACCAGTGGCTTCCAGAGTGAAAATCATTCCAGAAA W I L G D V F I R E Y Y S V F D R A N N	2640
2641	TGGATCCTGGGGGATGTTTTCATCCGAGAGTATTACAGCGTCTTTGACAGGGCCAACAAC L V G L A K A I *	2700
2701	CTCGTGGGGCTGGCCAAAGCCATCTGAAAGCTT	2733

HindIII

HindIII

HindIII.PvuII.PstI.XhoI.SstI.XbaI.BamHI

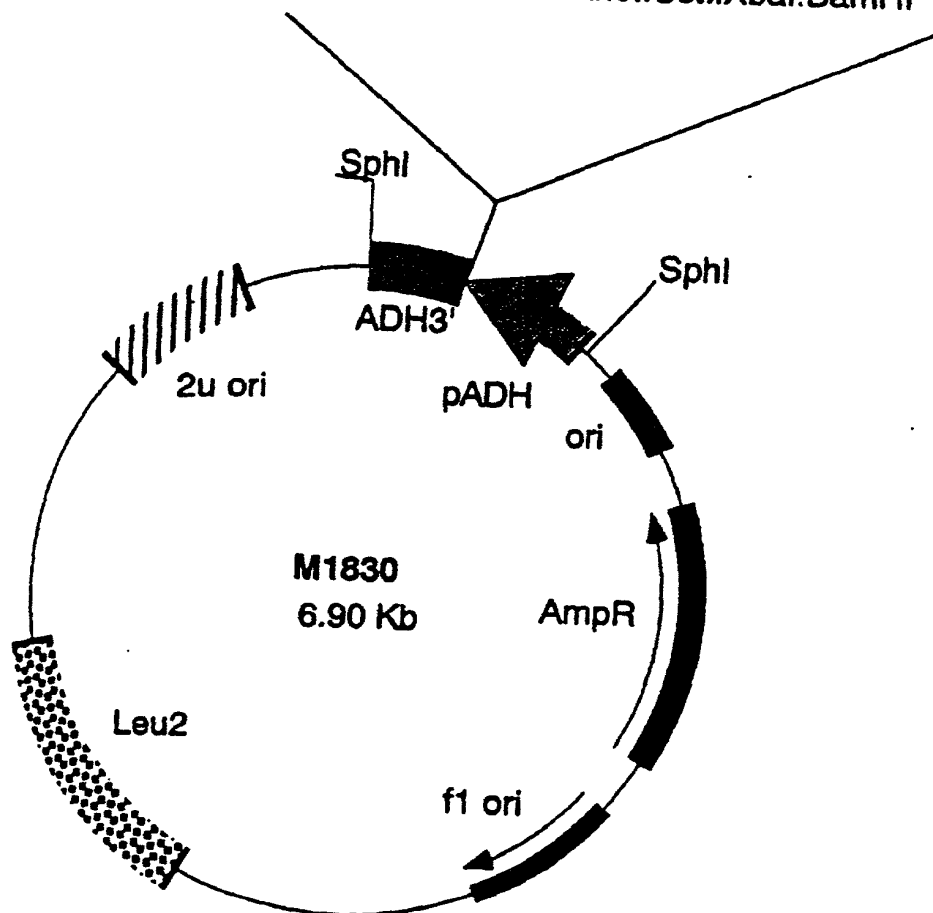


FIGURE 8

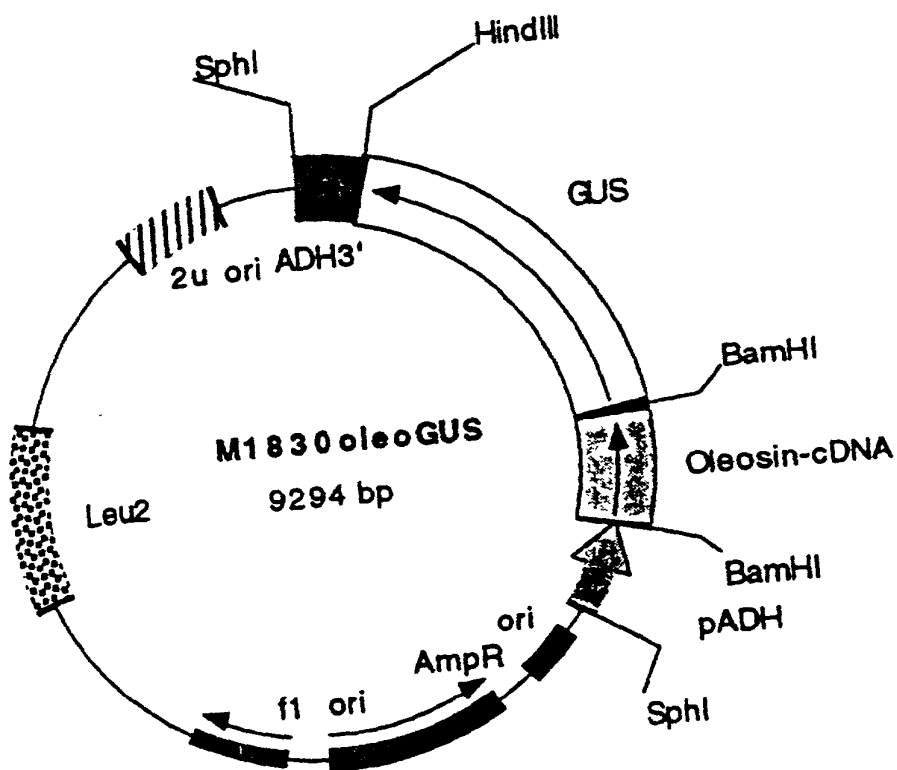


FIGURE 9

ClustalW Formatted Alignments

TR
ATTHIREDB

10 20 30 40 50 60

10 20 30 40 50 60

TR
ATTHIREDB

70 80 90 100 110 120

70 80 90 100 110 120

TR
ATTHIREDB

130 140 150 160 170 180

130 140 150 160 170 180

TR
ATTHIREDB

190 200 210 220 230 240

190 200 210 220 230 240

TR
ATTHIREDB

250 260 270 280 290 300

250 260 270 280 290 300

TR
ATTHIREDB

310 320 330 340 350 360

310 320 330 340 350 360

TR
ATTHIREDB

370 380 390 400 410 420

370 380 390 400 410 420

TR
ATTHIREDB

430 440 450 460 470 480

430 440 450 460 470 480

TR
ATTHIREDB

490 500 510 520 530 540

490 500 510 520 530 540

TR
ATTHIREDB

550 560 570 580 590 600

550 560 570 580 590 600

TR
ATTHIREDB

610 620 630 640 650 660

610 620 630 640 650 660

TR
ATTHIREDB

670 680 690 700 710 720

670 680 690 700 710 720

TR
ATTHIREDB

730 740 750 760 770 780

730 740 750 760 770 780

TR
ATTHIREDB

790 800 810 820 830 840

790 800 810 820 830 840

TR
ATTHIREDB

850 860 870 880 890 900

850 860 870 880 890 900

TR
ATTHIREDB

910 920 930 940 950 960

910 920 930 940 950 960

TR
ATTHIREDB

970 980 990 1000 1010 1020

970 980 990 1000 1010 1020

FIGURE 10

1	ATG	AAT	GGT	CTC	GAA	ACT	CAC	AAC	ACA	AGG	CTC	TGT	ATC	GTA	GGA	AGT	GGC	CCA	GCG	GCA	60
1	M	N	G	L	E	T	H	N	T	R	L	C	I	V	G	S	G	P	A	A	20
61	CAC	ACG	GCG	GCG	ATT	TAC	GCA	GCT	AGG	GCT	GAA	CTT	AAA	CCT	CTT	CTC	TTC	GAA	GGA	TGG	120
21	H	T	A	A	I	Y	A	A	R	A	E	L	K	P	L	L	F	E	G	W	40
121	ATG	GCT	AAC	GAC	ATC	GCT	CCC	GGT	GGT	CAA	CTA	ACA	ACC	ACC	ACC	GAC	GTC	GAG	AAT	TTC	180
41	M	A	N	D	I	A	P	G	G	Q	L	T	T	T	T	D	V	E	N	F	60
181	CCC	GGA	TTT	CCA	GAA	GGT	ATT	CTC	GGA	GTA	GAG	CTC	ACT	GAC	AAA	TTC	CGT	AAA	CAA	TCG	240
61	P	G	F	P	E	G	I	L	G	V	E	L	T	D	K	F	R	K	Q	S	80
241	GAG	CGA	TTC	GGT	ACT	ACG	ATA	TTT	ACA	GAG	ACG	GTG	ACG	AAA	GTC	GAT	TTC	TCT	TCG	AAA	300
81	E	R	F	G	T	T	I	F	T	E	T	V	T	K	V	D	F	S	S	K	100
301	CCG	TTT	AAG	CTA	TTC	ACA	GAT	TCA	AAA	GCC	ATT	CTC	GCT	GAC	GCT	GTG	ATT	CTC	GCT	ACT	360
101	P	F	K	L	F	T	D	S	K	A	I	L	A	D	A	V	I	L	A	T	120
361	GGA	GCT	GTG	GCT	AAG	CGG	CTT	AGC	TTC	GTT	GGA	TCT	GGT	GAA	GGT	TCT	GGA	GGT	TTC	TGG	420
121	G	A	V	A	K	R	L	S	F	V	G	S	G	E	G	S	G	G	F	W	140
421	AAC	CGT	GGA	ATC	TCC	GCT	TGT	GCT	GTT	TGC	GAC	GGA	GCT	GCT	CCG	ATA	TTC	CGT	AAC	AAA	480
141	N	R	G	I	S	A	C	A	V	C	D	G	A	A	P	I	F	R	N	K	160
481	CCT	CTT	GCG	GTG	ATC	GGT	GGA	GGC	GAT	TCA	GCA	ATG	GAA	GAA	GCA	AAC	TTT	CTT	ACA	AAA	540
161	P	L	A	V	I	G	G	G	D	S	A	M	E	E	A	N	F	L	T	K	180
541	TAT	GGA	TCT	AAA	GTG	TAT	ATA	ATC	CAT	AGG	AGA	GAT	GCT	TTT	AGA	GCG	TCT	AAG	ATT	ATG	600
181	Y	G	S	K	V	Y	I	I	H	R	R	D	A	F	R	A	S	K	I	M	200
601	CAG	CAG	CGA	GCT	TTG	TCT	AAT	CCT	AAG	ATT	GAT	GTG	ATT	TGG	AAC	TCG	TCT	GTT	GTG	GAA	660
201	Q	Q	R	A	L	S	N	P	K	I	D	V	I	W	N	S	S	V	V	E	220
661	GCT	TAT	GGA	GAT	GGA	GAA	AGA	GAT	GTG	CTT	GGA	GGA	TTG	AAA	GTG	AAG	AAT	GTG	GTT	ACC	720
221	A	Y	G	D	G	E	R	D	V	L	G	G	L	K	V	K	N	V	V	T	240
721	GGA	GAT	GTT	TCT	GAT	TTA	AAA	GTT	TCT	GGA	TTG	TTC	TTT	GCT	ATT	GGT	CAT	GAG	CCA	GCT	780
241	G	D	V	S	D	L	K	V	S	G	L	F	F	A	I	G	H	E	P	A	260
781	ACC	AAG	TTT	TTG	GAT	GGT	GGT	GTT	GAG	TTA	GAT	TCG	GAT	GGT	TAT	GTT	GTC	ACG	AAG	CCT	840
261	T	K	F	L	D	G	G	V	E	L	D	S	D	G	Y	V	V	T	K	P	280
841	GGT	ACT	ACA	CAG	ACT	AGC	GTT	CCC	GGA	GTT	TTC	GCT	GCG	GGT	GAT	GTT	CAG	GAT	AAG	AAG	900
281	G	T	T	Q	T	S	V	P	G	V	F	A	A	G	D	V	Q	D	K	K	300
901	TAT	AGG	CAA	GCC	ATC	ACT	GCT	GCA	GGA	ACT	GGG	TGC	ATG	GCA	GCT	TTG	GAT	GCA	GAG	CAT	960
301	Y	R	Q	A	I	T	A	A	G	T	G	C	M	A	A	L	D	A	E	H	320
961	TAC	TTA	CAA	GAG	ATT	GGA	TCT	CAG	CAA	GGT	AAG	AGT	GAT	TGA							1002
321	Y	L	Q	E	I	G	S	Q	Q	G	K	S	D	*							334

FIGURE 10

ClustalW Formatted Alignments

[illegible]

FIGURE 12

PstI

1 ctgcaggaattcattgtactcccagtatcattatagtgaaagtttggctctctcgccggtggtttttacctctattta 80

81 aaggggtttccacctaataattctggtatcattctcactttacttgttactttaattttctcataatctttggttgaaat 160

161 tatcacgcttcgcacacgatatccctacaaatttattatttggtaaacattttcaaaccgcataaaattttatgaagtc 240

241 ccgtctatctttaatgtagtctaacattttcatattgaaatatataatttacttaatttttagcgttggttagaagcataa 320

321 tgatttattcttattcttcttcatataaatgtttaatatataaataaaattctttaccttaagaaggatttcccat 400

401 tttatattttaaaaatatatttatcaaataattttcaaccacgtaaatctcataataataagttgtttcaaaagtaataa 480

481 aatttaactccataatttttttattcgactgatcttaaagcaacaccagtgacacaactagccattttttctttgaat 560

561 aaaaaaatccaattatcattgtatttttttatacaatgaaaatttcaccaaacaatcatttgggtatttctgaagcaa 640

641 gtcattgttatgcaaaattctataattcccatgtgacactacggaagtaactgaagatctgcttttacatgcgagacacat 720

721 cttctaaagtaattttaataatagttactatatattcaagatttcataatcaataactcaatattacttctaaaaattaa 800

801 ttagatataaataaataattacttttttaattttaagtttaattgttgaaattgtgactattgatttattattctactat 880

881 gtttaaattgttttatagatagtttaaagtaataataagtaatgtagtagagtgtagagtggtaccctaaccataaac 960

961 tataagatttatgggtggactaattttcatatatttcttattgcttttacctttcttgggtatgtaagtcggttaactggaa 1040

1041 ttactgtgggttgccatggcactctgtggtcttttggttcattgcatggatgcttgcgcaagaaaaagacaaagaacaaag 1120

1121 aaaaaagacaaaacagagagacaaaacgcaatcacacaaccaactcaaattagtcactgggtgatcaagatcgccgcgtc 1200

1201 catgtatgtctaaatgccatgcaaagcaacacgtgcttaacatgcactttaaatgggtcacccatctcaaccacacaca 1280

1281 aacacattgcctttttcttcatcatcaccacaaccacctgtatatattcattctcttcgccacctcaatttcttcactt 1360

1361 caacacacgtcaacctgcataatgcgtgtcatcccatgcccaaatctccatgcatgttccaaccaccttctctcttatata 1440

1441 atacctataaataacctctaataatcactcacttctttcatcatccatccatccagagtactactactctactactataata 1520

1521 ccccaacccaactcatattcaataactactctact ATG GCT TCG GAA GAA GGA CAA GTG ATC GCC TGC 1587

1 M A S E E G Q V I A C 11

1588 CAC ACC GTT GAG ACA TGG AAC GAG CAG CTT CAG AAG GCT AAT GAA TCC AAA ACT CTT GTG 1647

12 H T V E T W N E Q L Q K A N E S K T L V 31

1648 GTG GTT GAT TTC ACG GCT TCT TGG TGT GGA CCA TGT CGT TTC ATC GCT CCA TTC TTT GCT 1707

32 V V D F T A S W C G P C R F I A P F F A 51

1708 GAT TTG GCT AAG AAA CTT CCT AAC GTG CTT TTC CTC AAG GTT GAT ACT GAT GAA TTG AAG 1767

52 D L A K K L P N V L F L K V D T D E L K 71

FIGURE 12 (CONT'D)

1768	TCG GTG GCA AGT GAT TGG GCG ATA CAG GCG ATG CCA ACC TTC ATG TTT ATG AAG GAA GGG	1827
72	S V A S D W A I Q A M P T F M F L K E G	91
1828	AAG ATT TTG GAC AAA GTT GTT GGA GCC AAG AAA GAT GAG CTT CAG TCT ACC ATT GCC AAA	1887
92	K I L D K V V G A K K D E L Q S T I A K	111
	HindIII	
1888	CAC TTG GCT <u>TAA gctt</u> aataagtatgaactaaaatgcatgtaggtgtaagagctcatggagagcatggaatattgt	1963
112	H L A *	115
1964	atccgaccatgtaacagttataataactgagctccatctcacttcttctatgaataaacaaggatgttatgatatttaa	2043
2044	cactctatctatgacacctattgttctatgataaatttcctcttattattataaatcatctgaatcgtgacggcttatgg	2123
2124	aatgcttcaaatagtacaaaaacaattgtgtactataagactttctaaacaattctaaactttagcattgtgaacgagaca	2203
2204	taagtgttaagaagacataacaattataatggaagaagtttgtctccatttatatttatattaccacacttatgtatt	2283
2284	atattaggatgttaaggagacataacaattataaaagagagaagtttgtatccatttatatttatataactaccacatttat	2363
2364	atattatacttatccacttattttaatgtctttataaaggtttgatccatgatatttctaatatttttagttgatatttat	2443
2444	gaaaggttactatttgaactctcttactctgtataaaggttggatcatccttaaagtggtctattttaattttattgctt	2523
2524	cttacagataaaaaaaaaaattatgagttgggtttgataaaatattgaggattttaaaataataataaataaataaacat	2603
2604	ataatatatgtatataaatttattataatataacatttatctataaaaaagtaaatattgtcataaatctatacaatcgt	2683
2684	ttagccttgctggacgactctcaattattttaaacgagagtaaacatatttgactttttgggtattttaacaaattattatt	2763
2764	taacactatatgaaatttttttttttatcggaaggaaataaaaattaaattaggagggacaatggtgtgtcccaatcct	2843
2844	tatacaaccaacttccacaggaaggtcaggtcggggacaacaaaaaacaggcaagggaattttttaatttgggtgtgc	2923
2924	ttgtttgctgcataatttatgcagtaaaacactacacataacccttttagcagtagagcaatggttgaccgtgtgettag	3003
3004	cttctttttattttatttttttatcagcaagaataaaataaaataaaatgagacacttcagggatgtttcaacccttatac	3083
3084	aaaacccccaaaaacaagtttcttagcacccctaccaactaaggtagc	3129

FIGURE 13

PstI

1 ctgcaggaattcattgtactcccagtatcattatagtgaaagtttggctctctcgccggtggtttttacctctattta 80

81 aagggttttccacctaaaaattctggtatcattctcactttacttgttactttaattctcataatctttggttgaaat 160

161 tatcacgcttccgcacacgatatccctacaaatttattatttgttaaacattttcaaaccgcataaaattttatgaagtc 240

241 ccgtctatctttaatgtagtctaacattttcatattgaaatatataatttacttaatttttagcgttggttagaaagcataa 320

321 tgatttattcttattcttcttcatataaagttaaataacaataaacaattctttacottaagaaggatttcccat 400

401 tttatattttaaaaatatatttatcaaatatttttaaccacgtaaatctcataataataagttgtttcaaaagtaataa 480

481 aatttaactccataatttttttattcgactgatcttaaagcaacacccagtgacacaactagccattttttctttgaat 560

561 aaaaaaatccaattatcattgtatttttttatacaatgaaaatttcaccaaacaatcatttgggtattttctgaagcaa 640

641 gtcatgttatgcaaaattctataattcccatgtgacactacggaagtaactgaagatctgcttttacatgcgagacacat 720

721 cttctaaagtaattttaataatagttactatattcaagatttcatatatcaataactcaatattacttctaaaaaattaa 800

801 ttagatataaattaaatattacttttttaattttaagtttaattgttgaatttgtgactattgatttattattctactat 880

881 gtttaaattgttttatagatagtttaaagtaaatataagtaatgtagtagagtgttagagtgttacctaaccataaac 960

961 tataagatttatggtggactaattttcatatatttcttattgcttttaccttttcttggtatgtaagtcgtaactggaa 1040

1041 ttactgtgggttgccatggcactctgtggtcttttggttcatgcatggatgcttgcgcaagaaaagacaaagaacaaag 1120

1121 aaaaaagacaaaacagagagacaaaacgcaatcacacaaccaactcaaattagtcactggctgatcaagatcgccgcgtc 1200

1201 catgtatgtctaaatgccatgcaaagcaacacgtgcttaacatgcactttaaatggctcaccatctcaaccacacaca 1280

1281 aacacattgocctttttcttcatcatcaccacaaccacotgtatatattcattctcttccgccacctcaatttcttcaactt 1360

1361 caacacacgtcaacctgcatatgcgtgtcatcccatgccaaatctccatgcatgttccaaccaccttctcttattata 1440

1441 atacctataaatacctctaataatcactcacttctttcatcatccatccagagtactactctactactataata 1520

1521 ccccaaccaactcatattcaatactactctact ATG GCG GAT ACA GCT AGA GGA ACC CAT CAC GAT 1587

1 M A D T A R G T H H D 11

1588 ATC ATC GGC AGA GAC CAG TAC CCG ATG ATG GGC CGA GAC CGA GAC CAG TAC CAG ATG TCC 1647

12 I I G R D Q Y P M M G R D R D Q Y Q M S 31

1648 GGA CGA GGA TCT GAC TAC TCC AAG TCT AGG CAG ATT GCT AAA GCT GCA ACT GCT GTC ACA 1707

32 G R G S D Y S K S R Q I A K A A T A V T 51

1708 GCT GGT GGT TCC CTC CTT GTT CTC TCC AGC CTT ACC CTT GTT GGA ACT GTC ATA GCT TTG 1767

52 A G G S L L V L S S L T L V G T V I A L 71

1768	ACT	GTT	GCA	ACA	CCT	CTG	CTC	GTT	ATC	TTC	AGC	CCA	ATC	CTT	GTC	CCG	GCT	CTC	ATC	ACA	1827													
72	T	V	A	T	P	L	L	V	I	F	S	P	I	L	V	P	A	L	I	T	91													
1828	GTT	GCA	CTC	CTC	ATC	ACC	GGT	TTT	CTT	TCC	TCT	GGA	GGG	TTT	GGC	ATT	GCC	GCT	ATA	ACC	1887													
92	V	A	L	L	I	T	G	F	L	S	S	G	G	F	G	I	A	A	I	T	111													
1888	GTT	TTC	TCT	TGG	ATT	TAC	AA	<i>gtaagcacacatttatcatcttacttcataat</i>												<i>ttgtgcaatatgtgcatgca</i>	1960													
112	V	F	S	W	I	Y	K														118													
1961	<i>tgtgttgagccagtagcctttggatcaat</i>																				<i>tttttggtcgaataacaaatgtaacaataagaaattgcaaattc</i>	<i>tagggaa</i>	2040											
2041	<i>catttgggttaactaaatacgaaatttgacctagcttagccttgaatgtgtcgtgtatatcatctatataggtaaaatgctt</i>																				2120													
2121	<i>ggatatgatacctatttgattgtgaatag</i>																				G	TAC	GCA	ACG	GGA	GAG	CAC	CCA	CAG	GGA	TCA	GAC	AAG	2184
119																					Y	A	T	G	E	H	P	Q	G	S	D	K	130	
2185	TTG	GAC	AGT	GCA	AGG	ATG	AAG	TTG	GGA	AGC	AAA	GCT	CAG	GAT	CTG	AAA	GAC	AGA	GCT	CAG	2244													
131	L	D	S	A	R	M	K	L	G	S	K	A	Q	D	L	K	D	R	A	Q	150													
2245	TAC	TAC	GGA	CAG	CAA	CAT	ACT	GGT	GGG	GAA	CAT	GAC	CGT	GAC	CGT	ACT	CGT	GGT	GGC	CAG	2304													
151	Y	Y	G	Q	Q	H	T	G	G	E	H	D	R	D	R	T	R	G	G	Q	170													
	NcoI																																	
2305	CAC	ACT	<u>ACC</u>	<u>ATG</u>	GCT	TCG	GAA	GAA	GGA	CAA	GTG	ATC	GCC	TGC	CAC	ACC	GTT	GAG	ACA	TGG	2364													
171	H	T	T	M	A	S	E	E	G	Q	V	I	A	C	H	T	V	E	T	W	190													
2365	AAC	GAG	CAG	CTT	CAG	AAG	GCT	AAT	GAA	TCC	AAA	ACT	CTT	GTG	GTG	GTT	GAT	TTC	ACG	GCT	2424													
191	N	E	Q	L	Q	K	A	N	E	S	K	T	L	V	V	V	D	F	T	A	210													
2425	TCT	TGG	TGT	GGA	CCA	TGT	CGT	TTC	ATC	GCT	CCA	TTC	TTT	GCT	GAT	TTG	GCT	AAG	AAA	CTT	2484													
211	S	W	C	G	P	C	R	F	I	A	P	F	F	A	D	L	A	K	K	L	230													
2485	CCT	AAC	GTG	CTT	TTC	CTC	AAG	GTT	GAT	ACT	GAT	GAA	TTG	AAG	TCG	GTG	GCA	AGT	GAT	TGG	2544													
231	P	N	V	L	F	L	K	V	D	T	D	E	L	K	S	V	A	S	D	W	250													
2545	GCG	ATA	CAG	GCG	ATG	CCA	ACC	TTC	ATG	TTT	TTG	AAG	GAA	GGG	AAG	ATT	TTG	GAC	AAA	GTT	2604													
251	A	I	Q	A	M	P	T	F	M	F	L	K	E	G	K	I	L	D	K	V	270													
2605	GTT	GGA	GCC	AAG	AAA	GAT	GAG	CTT	CAG	TCT	ACC	ATT	GCC	AAA	CAC	TTG	GCT	<u>TAA</u>	<u>gcttaata</u>	2666														
271	V	G	A	K	K	D	E	L	Q	S	T	I	A	K	H	L	A	*		288														
2667	<i>agtatgaactaaaatgcatgtaggtgtaagagctcatggagagcatggaatattgtatccgacctgtaacagtataata</i>																				2746													
2747	<i>actgagctccatctcacttcttctatgaataaacaaggatgttatgatataattaacactctatctatgcaccttattgt</i>																				2826													
2827	<i>tctatgataaatttcttcttattattataaatcatctgaatcgtgacggttatggaatgcttcaaatagtacaaaaaca</i>																				2906													
2907	<i>aatgtgtactataagacttttctaacaattctaacttttagcattgtgaacgagacataagtgttaagaagacataacaat</i>																				2986													
2987	<i>tataatggaagaagtttgtctccatttatattatatattaccacttatgtattatattaggatgttaaggagacata</i>																				3066													

FIGURE 13 (CONT'D)

3067	acaattataaagagagagaagtttgatatccatttatatattatatactactaccatttatatattacttattccacttatttta	3146
3147	atgtcttttataaggtttgatccatgatattttctaataatttttagttgatatgtatatgaaaggggtactatttgaactctct	3226
3227	tactctgtataaaggttggtatcatccttaaagtgggtctattttaattttattgtctcttacagataaaaaaaaaaattatg	3306
3307	agttggtttgataaaatattgaaggattttaaataataataaataaataaataacatataatatatgtatataaaatttatt	3386
3387	ataatataacattttatctataaaaaagtaaatattgtcataaatctatacaatcgtttagccttgctggacgactctcaa	3466
3467	ttattttaaacgagagtaaacatatttgactttttggttatttaacaaattattatttaacactatatgaaattttttttt	3546
3547	tttatcggaaggaaataaaattaaattaggaggggacaatgggtgtgtcccaatccttatacaaccaacttccacaggaag	3626
3627	gtcaggtcggggacaacaaaaaacagggaagggaattttttaatttggggtgtcttgtttgctgcataatttatgcag	3706
3707	taaaacactacacataacccttttagcagtagagcaatggttgaccgtgtgcttagcttcttttatttttatttttttatc	3786
3787	agcaaagaataaaaaataaaaatgagacacttcagggatgtttcaacccttatacaaaacccccaaaaacaagtttccta	3866
3867	gcaccctaccaactaaggtacc	3888

KpnI

FIGURE 14

PstI

1 ctgcaggaattcattgtactcccagtatcattatagtgaaagtttggctctctcgccggtgggtttttacctctattta 80

81 aaggggttttccacctaataattctggtatcattctcactttacttggtactttaattttctcataatctttggttgaaat 160

161 tatcacgcttcgcgacacgatatccctacaaatttattatttggttaaacattttcaaaccgcataaaaattttatgaagtc 240

241 ccgtctatctttaatgtagcttaacattttcatattgaaatatataatttacttaatttttagcggttggtagaagcataa 320

321 tgatttattctttattctttctcatataaatgtttaataatacaataaacaattctttaccttaagaaggatttcccat 400

401 tttatattttaaaaatatatttatcaaataattttcaaccacgtaaatctcataataataagttgtttcaaaagtaataa 480

481 aatttaactocataatttttttattcgactgatcttaagcaacacccagtgacacaaactagccattttttctttgaat 560

561 aaaaaaatccaattatcattgtatttttttatacaatgaaaatttcaccaaacaatcatttggtgtatttctgaagcaa 640

641 gtcattgttatgcaaaattctataattccatttgacactacggaagtaactgaagatctgcttttacatgcgagacacat 720

721 cttctaaagtaattttaataatagttactatattcaagatttcatatatcaaatactcaatattacttctaaaaaattaa 800

801 ttagatataattaaaaattacttttttaattttaagtttaattggtgaatttggtgactattgatttattattctactat 880

881 gtttaaattgttttatagatagtttaaagtaaatataagtaagttagtagtgtagtggttagagtggttacctaaccataaac 960

961 tataagatttattggtggactaattttcatatatttcttattgctttttaccttttcttggtatgtaagtcgtaactggaa 1040

1041 ttactgtgggttgccatggcactctgtggtcttttggttcatgcatggatgcttgcgcaagaaaaagacaaagaacaaag 1120

1121 aaaaaagacaaaacagagagacaaaacgcaatcacacaaccaactcaaattagtcactggctgatcaagatcgccgcgctc 1200

1201 catgtatgtctaaatgccatgcaaagcaacacgtgcttaacatgcacttttaaatggctcaccatctcaaccacacaca 1280

1281 aacacattgcctttttttcatcatcaccacaaccacctgtatatattcattctcttcgccacctcaatttcttctactt 1360

1361 caacacacgtcaacctgcatatgcgtgtcatcccatgcccaaatctccatgcatgttccaaccaccttctctcttatata 1440

1441 atacctataaataacctctaataatcactcacttctttcatcatccatccatccagagtactactactctactactataata 1520

1521 ccccaacccaactcatattcaataactactctact ATG GCT TCG GAA GAA GGA CAA GTG ATC GCC TGC 1587

1 M A S E E G Q V I A C 11

1588 CAC ACC GTT GAG ACA TGG AAC GAG CAG CTT CAG AAG GCT AAT GAA TCC AAA ACT CTT GTG 1647

12 H T V E T W N E Q L Q K A N E S K T L V 31

1648 GTG GTT GAT TTC ACG GCT TCT TGG TGT GGA CCA TGT CGT TTC ATC GCT CCA TTC TTT GCT 1707

32 V V D F T A S W C G P C R F I A P F F A 51

1708 GAT TTG GCT AAG AAA CTT CCT AAC GTG CTT TTC CTC AAG GTT GAT ACT GAT GAA TTG AAG 1767

52 D L A K K L P N V L F L K V D T D E L K 71

FIGURE 14 (CONT'D)

1768	TCG GTG GCA AGT GAT TGG GCG ATA CAG GCG ATG CCA ACC TTC ATG TTT TTG AAG GAA GGG	1827
72 S V A S D W A I Q A M P T F M F L K E G	91	
1828	AAG ATT TTG GAC AAA GTT GTT GGA GCC AAG AAA GAT GAG CTT CAG TCT ACC ATT GCC AAA	1887
92 K I L D K V V G A K K D E L Q S T I A K	111	
1888	CAC TTG GCT ATG GCG GAT ACA GCT AGA GGA ACC CAT CAC GAT ATC ATC GGC AGA GAC CAG	1947
112 H L A M A D T A R G T H H D I I G R D Q	131	
1948	TAC CCG ATG ATG GGC CGA GAC CGA GAC CAG TAC CAG ATG TCC GGA CGA GGA TCT GAC TAC	2007
132 Y P M M G R D R D Q Y Q M S G R G S D Y	151	
2008	TCC AAG TCT AGG CAG ATT GCT AAA GCT GCA ACT GCT GTC ACA GCT GGT GGT TCC CTC CTT	2067
152 S K S R Q I A K A A T A V T A G G S L L	171	
2068	GTT CTC TCC AGC CTT ACC CTT GTT GGA ACT GTC ATA GCT TTG ACT GTT GCA ACA CCT CTG	2127
172 V L S S L T L V G T V I A L T V A T P L	191	
2128	CTC GTT ATC TTC AGC CCA ATC CTT GTC CCG GCT CTC ATC ACA GTT GCA CTC CTC ATC ACC	2187
192 L V I F S P I L V P A L I T V A L L I T	211	
2188	GGT TTT CTT TCC TCT GGA GGG TTT GGC ATT GCC GCT ATA ACC GTT TTC TCT TGG ATT TAC	2247
212 G F L S S G G F G I A A I T V F S W I Y	231	
2248	AA gtaagcacacatttatcatcttacttcataaatTTTTgtgcaatatgtgcacatgtgttgagccagtagcctttggat	2326
232 K	232	
2327	caatTTTTTtggtcgaaataacaaaatgtaacaataagaaattgcaaattctagggaacatttggttaactaataacgaaat	2406
2407	ttagacctagctagcttgaatgtgtctgtgtatatcatctatataggtaaaaatgcttggatgatacctattgattgtgaa	2486
2487	tag G TAC GCA ACG GGA GAG CAC CCA CAG GGA TCA GAC AAG TTG GAC AGT GCA AGG ATG	2544
233 Y A T G E H P Q G S D K L D S A R M	250	
2545	AAG TTG GGA AGC AAA GCT CAG GAT CTG AAA GAC AGA GCT CAG TAC TAC GGA CAG CAA CAT	2604
251 K L G S K A Q D L K D R A Q Y Y G Q Q H	270	
	HindIII	
2605	ACT GGT GGG GAA CAT GAC CGT GAC CGT ACT CGT GGT GGC CAG CAC ACT ACT TAA gctttaata	2666
271 T G G E H D R D R T R G G Q H T T *	288	
2667	agtatgaactaaaaatgcatgtaggtgtaagagctcatggagagcatggaatattgtatccgaccatgtaacagttataata	2746
2747	actgagctccatctcacttcttcttatgaataaacaaggatgttatgatataattaacactctatctatgcaccttattgt	2826
2827	tctatgataaaatttcctcttattattataaaatcatctgaatcgtgacggcttatggaatgcttcaaatagtacaaaaaca	2906
2907	aatgtgtactataagactttctaacaattctaacttttagcatttgtgaacgagacataagtgttaagaagacataacaat	2986
2987	tataatggaagaagtttgtctccatttatatattatatattaccacttatgtattatattaggtgttaaggagacata	3066

FIGURE 14 (CONT'D)

FIGURE 15

PstI

1 ctgcaggaattcattgtactcccagtatcattatagtgaaagttttggctctctcgccggtgggtttttacctctattta 80
81 aaggggttttccacctaataattctggtatcattctcactttacttggtactttaattttctcataatctttggttgaaat 160
161 tatcacgcttccgcacacgatccctacaaatttattatttgtaaaccattttcaaaccgcataaaattttatgaagtc 240
241 ccgtctatctttaatgtagtctaaccattttcatattgaaatatataatttacttaatttttagcggttggtagaagcataa 320
321 tgatttattcttattcttcttcatataaatgtttaatatataaacaattctttaccttaagaaggatttcccat 400
401 ttatatttttaaaatatatttatcaaataattttcaaccacgtaaattctcataataataagttgtttcaaaagtaataa 480
481 aatttaactccataatttttttattcgactgatcttaagcaacacccagtgacacaactagccattttttctttgaat 560
561 aaaaaaatccaattatcattgtatttttttataacaatgaaaatttcaccaaacaatcatttggtggtattttctgaagcaa 640
641 gtcattgttatgcaaaattctataattccatttgacactacggaagtaactgaagatctgcttttacatgcgagacacat 720
721 ctcttaaagtaattttaataatagttactatattcaagatttcatatatcaaatactcaatattacttctaaaaaattaa 800
801 ttagatataattaaaatattacttttttaattttaagtttaattgttgatttgactattgatttattattctactat 880
881 gtttaaattgttttatagatagtttaaagtaaatataagtaagttagtagtgtagtggttagagtggtaccctaaaccataaac 960
961 tataagatttatggtggactaattttcatatatttcttattgcttttaccttttcttggtatgtaagtcgtaactggaa 1040
1041 ttactgtgggttgccatggcactctgtggtcttttggttcatgcatggatgcttgcgcaagaaaagacaaagaacaaag 1120
1121 aaaaaagacaaaacagagagacaaaacgcaatcacacaaccaactcaaattagtcactggctgatcaagatcgccgcgtc 1200
1201 catgtatgtctaaatgccatgcaaagcaacacgtgcttaacatgcactttaaatgggtcacccatctcaaccacacaca 1280
1281 aacacattgcctttttcttcatcatcaccacaaccacctgtatatattcattctcttccgccacctcaatttcttcaactt 1360
1361 caacacacgtcaacctgcataatgcgtgtcatcccatgccc aaatctccatgcatgttccaaccacettctctcttatata 1440
1441 atacctataaataacctctaataatcactcacttctttcatcatccatccatccagagtactactactctactactataata 1520
1521 ccccaaccaactcatattcaataactactctact ATG AAT GGT CTC GAA ACT CAC AAC ACA AGG CTC 1587
1 M N G L E T H N T R L 11
1588 TGT ATC GTA GGA AGT GGC CCA GCG GCA CAC ACG GCG GCG ATT TAC GCA GCT AGG GCT GAA 1647
12 C I V G S G P A A H T A A I Y A A R A E 31
1648 CTT AAA CCT CTT CTC TTC GAA GGA TGG ATG GCT AAC GAC ATC GCT CCC GGT GGT CAA CTA 1707
32 L K P L L F E G W M A N D I A P G G Q L 51
1708 ACA ACC ACC ACC GAC GTC GAG AAT TTC CCC GGA TTT CCA GAA GGT ATT CTC GGA GTA GAG 1767
52 T T T T D V E N F P G F P E G I L G V E 71

FIGURE 15 (CONT'D)

1768 CTC ACT GAC AAA TTC CGT AAA CAA TCG GAG CGA TTC GGT ACT ACG ATA TTT ACA GAG ACG 1827
72 L T D K F R K Q S E R F G T T I F T E T 91

1828 GTG ACG AAA GTC GAT TTC TCT TCG AAA CCG TTT AAG CTA TTC ACA GAT TCA AAA GCC ATT 1887
92 V T K V D F S S K P F K L F T D S K A I 111

1888 CTC GCT GAC GCT GTG ATT CTC GCT ACT GGA GCT GTG GCT AAG CGG CTT AGC TTC GTT GGA 1947
112 L A D A V I L A T G A V A K R L S F V G 131

1948 TCT GGT GAA GGT TCT GGA GGT TTC TGG AAC CGT GGA ATC TCC GCT TGT GCT GTT TGC GAC 2007
132 S G E G S G G F W N R G I S A C A V C D 151

2008 GGA GCT GCT CCG ATA TTC CGT AAC AAA CCT CTT GCG GTG ATC GGT GGA GGC GAT TCA GCA 2067
152 G A A P I F R N K P L A V I G G G D S A 171

2068 ATG GAA GAA GCA AAC TTT CTT ACA AAA TAT GGA TCT AAA GTG TAT ATA ATC CAT AGG AGA 2127
172 M E E A N F L T K Y G S K V Y I I H R R 191

2128 GAT GCT TTT AGA GCG TCT AAG ATT ATG CAG CAG CGA GCT TTG TCT AAT CCT AAG ATT GAT 2187
192 D A F R A S K I M Q Q R A L S N P K I D 211

2188 GTG ATT TGG AAC TCG TCT GTT GTG GAA GCT TAT GGA GAT GGA GAA AGA GAT GTG CTT GGA 2247
212 V I W N S S V V E A Y G D G E R D V L G 231

2248 GGA TTG AAA GTG AAG AAT GTG GTT ACC GGA GAT GTT TCT GAT TTA AAA GTT TCT GGA TTG 2307
232 G L K V K N V V T G D V S D L K V S G L 251

2308 TTC TTT GCT ATT GGT CAT GAG CCA GCT ACC AAG TTT TTG GAT GGT GGT GTT GAG TTA GAT 2367
252 F F A I G H E P A T K F L D G G V E L D 271

2368 TCG GAT GGT TAT GTT GTC ACG AAG CCT GGT ACT ACA CAG ACT AGC GTT CCC GGA GTT TTC 2427
272 S D G Y V V T K P G T T Q T S V P G V F 291

2428 GCT GCG GGT GAT GTT CAG GAT AAG AAG TAT AGG CAA GCC ATC ACT GCT GCA GGA ACT GGG 2487
292 A A G D V Q D K K Y R Q A I T A A G T G 311

2488 TGC ATG GCA GCT TTG GAT GCA GAG CAT TAC TTA CAA GAG ATT GGA TCT CAG CAA GGT AAG 2547
312 C M A A L D A E H Y L Q E I G S Q Q G K 331

2548 AGT GAT TGA agctttaataagtatgaactaaaatgcatgtaggtgtaagagctcatggagagcatggaatattgtatc 2624
332 S D * HindIII 334

2625 cgaccatgtaacagtataataaactgagctccatctcacttcttctatgaataaacaaggatgttatgatatattaacac 2704

2705 tctatctatgcaccttattgttctatgataaaatttctcttattattataaaatcatctgaatcgtgacggccttatggaat 2784

2785 gcttcaaatagtacaaaaacaatgtgtactataagactttctaaacaattctaacttttagcattgtgaacgagacataa 2864

2865 gtgttaagaagacataacaattataatggaagaagttgtctccatttatattatatattaccacttatgtattata 2944

034547-0106

FIGURE 15 (CONT'D)

2945 ttaggatgttaaggagacataacaattataaagagagaagtttgatccatttatattatataactaccatttatata 3024
3025 ttatacttatccacttatttaagtgtctttataagggttgatccatgatatttctaataattttagttgatatgtatatgaa 3104
3105 aggggtactatttgaactctcttactctgtataaagggtggatcatccttaaagtgggtctatttaattttattgcttctt 3184
3185 acagataaaaaaaaaattatgagttgggttgataaaatattgaaggatttaaataataataataataataacatata 3264
3265 atatatgtatataaatttattataaatataacatttatctataaaaaagtaaataattgtcataaatctatacaatcgttta 3344
3345 gccttgctggacgactctcaattatttaaacgagagtaaacatatattgactttttgggttatttaacaaattattatttaa 3424
3425 cactatatgaaatTTTTTTTTTTTatcggcaaggaaataaaattaaattaggagggacaatgggtgtgtcccaatccttat 3504
3505 acaaccaacttccacaggaaggtcaggtcggggacaacaaaaaacaggcaagggaatttttaatttgggttgctcttg 3584
3585 ttgctgcataatttatgcagtaaaacactacacataacccttttagcagtagagcaatggttgaccgtgtgcttagctt 3664
3665 cttttatttttttttttttatcagcaaagaataaaataaaatgagacacttcagggatgtttcaacccttatacaaa 3744
3745 accccaaaaacaagtttctagcacctaccaactaagggtacc 3787

KpnI

FIG 15 CONT'D

FIGURE 16

PstI

1 ctgcaggaattcattgtactcccagtatcattatagtgaaagttttggctctctcgccggtgggtttttacctctattta 80

81 aaggggttttccacctaataaattctggtatcattctcactttacttggtactttaatttctcataatctttggttgaaat 160

161 tatcacgcttccgcacacgatatccctacaaatttattatttggttaaacattttcaaaccgcataaaattttatgaagtc 240

241 ccgtctatctttaatgtagtctaacattttcatattgaaatatataatttacttaatttttagcggtggtagaagcataa 320

321 tgatttattcttattcttcttcatataaatgtttaatatataaataaacaattctttaccttaagaaggatttcccat 400

401 tttatattttaaaaaatatatttatcaaataattttcaaccacgtaaattctcataataataagttgtttcaaaagtaataa 480

481 aatttaactccataatttttttattcgactgatcttaagcaacacccagtgacacaactagccattttttctttgaat 560

561 aaaaaaatccaattatcattgtatttttttatacaatgaaaatttcaccaaacaatcatttgggtatttctgaagcaa 640

641 gtcattgtatgcaaaattctataattccatttgacactacggaagtaactgaagatctgcttttcatgagagacacat 720

721 cttctaaagtaattttaataatagttactatattcaagatttcataatcaataactcaatattacttctaaaaaattaa 800

801 ttagatataaataaataattacttttttaattttaagtttaattgttggaatttgactattgatttattattctactat 880

881 gtttaaatgtttttatagatagtttaagtaaatataagtaatgtagtagagtgttagagtgttacccctaaaccataaac 960

961 tataagattttatggtggactaattttcatatatttcttattgctttttaccttttcttggtatgtaagtcgtaactggaa 1040

1041 ttactgtgggttgccatggcactctgtggtcttttggttcatgcatggatgcttgcgcaagaaaaagacaaagaacaaag 1120

1121 aaaaaagacaaaacagagagacaaaacgcaatcacacaaccaactcaaattagtcactggctgatcaagatcgccgcgtc 1200

1201 catgtatgtctaaatgccatgcaaagcaacacgtgcttaacatgcactttaaatggctcaccatctcaaccacacaca 1280

1281 aacacattgccttttttctcatcatcaccacaaccacctgtatatattcattctcttcgccacctcaatttcttcactt 1360

1361 caacacacgtcaacctgcataatgcgtgtcatcccatgccaaatctccatgcatgttccaaccaccttctctcttatata 1440

1441 atacctataaataacctctaataatcactcacttctttcatcatccatccatccagagtactactactactactataata 1520

1521 cccaacccaactcatattcaataactactctact ATG GCG GAT ACA GCT AGA GGA ACC CAT CAC GAT 1587

1 M A D T A R G T H H D 11

1588 ATC ATC GGC AGA GAC CAG TAC CCG ATG ATG GGC CGA GAC CGA GAC CAG TAC CAG ATG TCC 1647

12 I I G R D Q Y P M M G R D R D Q Y Q M S 31

1648 GGA CGA GGA TCT GAC TAC TCC AAG TCT AGG CAG ATT GCT AAA GCT GCA ACT GCT GTC ACA 1707

32 G R G S D Y S K S R Q I A K A A T A V T 51

1708 GCT GGT GGT TCC CTC CTT GTT CTC TCC AGC CTT ACC CTT GTT GGA ACT GTC ATA GCT TTG 1767

FIGURE 16 (CONT'D)

52 A G G S L L V L S S L T L V G T V I A L 71

1768 ACT GTT GCA ACA CCT CTG CTC GTT ATC TTC AGC CCA ATC CTT GTC CCG GCT CTC ATC ACA 1827
72 T V A T P L L V I F S P I L V P A L I T 91

1828 GTT GCA CTC CTC ATC ACC GGT TTT CTT TCC TCT GGA GGG TTT GGC ATT GCC GCT ATA ACC 1887
92 V A L L I T G F L S S G G F G I A A I T 111

1888 GTT TTC TCT TGG ATT TAC AA *gtaagcacacatttatcatcttacttcataattttgtgcaatatgtgcatgca* 1960
112 V F S W I Y K 118

1961 *tgtgttgagccagtagctttggatcaatttttttggtcgaataacaaatgtaacaataagaaattgcaaattctagggaa* 2040

2041 *catttggttaactaaatacgaatttgacctagctagcttgaatgtgtctgtgtatatcatctatataggtaaaatgctt* 2120

2121 *ggtatgatacctattgattgtgaatag* G TAC GCA ACG GGA GAG CAC CCA CAG GGA TCA GAC AAG 2184
119 Y A T G E H P Q G S D K 130

2185 TTG GAC AGT GCA AGG ATG AAG TTG GGA AGC AAA GCT CAG GAT CTG AAA GAC AGA GCT CAG 2244
131 L D S A R M K L G S K A Q D L K D R A Q 150

2245 TAC TAC GGA CAG CAA CAT ACT GGT GGG GAA CAT GAC CGT GAC CGT ACT CGT GGT GGC CAG 2304
151 Y Y G Q Q H T G G E H D R D R T R G G Q 170

2305 CAC ACT ACC ATG AAT GGT CTC GAA ACT CAC AAC ACA AGG CTC TGT ATC GTA GGA AGT GGC 2364
171 H T T M N G L E T H N T R L C I V G S G 190

2365 CCA GCG GCA CAC ACG GCG GCG ATT TAC GCA GCT AGG GCT GAA CTT AAA CCT CTT CTC TTC 2424
191 P A A H T A A I Y A A R A E L K P L L F 210

2425 GAA GGA TGG ATG GCT AAC GAC ATC GCT CCC GGT GGT CAA CTA ACA ACC ACC ACC GAC GTC 2484
211 E G W M A N D I A P G G Q L T T T T D V 230

2485 GAG AAT TTC CCC GGA TTT CCA GAA GGT ATT CTC GGA GTA GAG CTC ACT GAC AAA TTC CGT 2544
231 E N F P G F P E G I L G V E L T D K F R 250

2545 AAA CAA TCG GAG CGA TTC GGT ACT ACG ATA TTT ACA GAG ACG GTG ACG AAA GTC GAT TTC 2604
251 K Q S E R F G T T I F T E T V T K V D F 270

2605 TCT TCG AAA CCG TTT AAG CTA TTC ACA GAT TCA AAA GCC ATT CTC GCT GAC GCT GTG ATT 2664
271 S S K P F K L F T D S K A I L A D A V I 290

2665 CTC GCT ACT GGA GCT GTG GCT AAG CGG CTT AGC TTC GTT GGA TCT GGT GAA GGT TCT GGA 2724
291 L A T G A V A K R L S F V G S G E G S G 310

2725 GGT TTC TGG AAC CGT GGA ATC TCC GCT TGT GCT GTT TGC GAC GGA GCT GCT CCG ATA TTC 2784
311 G F W N R G I S A C A V C D G A A P I F 330

2785 CGT AAC AAA CCT CTT GCG GTG ATC GGT GGA GGC GAT TCA GCA ATG GAA GAA GCA AAC TTT 2844
331 R N K P L A V I G G G D S A M E E A N F 350

2025 RELEASE UNDER E.O. 14176

FIGURE 16 (CONT'D)

2845 CTT ACA AAA TAT GGA TCT AAA GTG TAT ATA ATC CAT AGG AGA GAT GCT TTT AGA GCG TCT 2904
351 L T K Y G S K V Y I I H R R D A F R A S 370

2905 AAG ATT ATG CAG CAG CGA GCT TTG TCT AAT CCT AAG ATT GAT GTG ATT TGG AAC TCG TCT 2964
371 K I M Q Q R A L S N P K I D V I W N S S 390

2965 GTT GTG GAA GCT TAT GGA GAT GGA GAA AGA GAT GTG CTT GGA GGA TTG AAA GTG AAG AAT 3024
391 V V E A Y G D G E R D V L G G L K V K N 410

3025 GTG GTT ACC GGA GAT GTT TCT GAT TTA AAA GTT TCT GGA TTG TTC TTT GCT ATT GGT CAT 3084
411 V V T G D V S D L K V S G L F F A I G H 430

3085 GAG CCA GCT ACC AAG TTT TTG GAT GGT GGT GTT GAG TTA GAT TCG GAT GGT TAT GTT GTC 3144
431 E P A T K F L D G G V E L D S D G Y V V 450

3145 ACG AAG CCT GGT ACT ACA CAG ACT AGC GTT CCC GGA GTT TTC GCT GCG GGT GAT GTT CAG 3204
451 T K P G T T Q T S V P G V F A A G D V Q 470

3205 GAT AAG AAG TAT AGG CAA GCC ATC ACT GCT GCA GGA ACT GGG TGC ATG GCA GCT TTG GAT 3264
471 D K K Y R Q A I T A A G T G C M A A L D 490

3265 GCA GAG CAT TAC TTA CAA GAG ATT GGA TCT CAG CAA GGT AAG AGT GAT TGA agcttaataaagt 3327
491 A E H Y L Q E I G S Q Q G K S D * HindIII 507

3328 atgaactaaatgcatgttaggtgtaagagctcatggagagcatggaatattgtatccgaccatgtaacagtataataact 3407

3408 gagctccatctcacttcttctatgaataaacaaggatgttatgatataataacactctatctatgcaccttattgttct 3487

3488 atgataaatttcttcttattattataaatcatctgaatcgtgacggcttatggaatgcttcaaatagtacaaaaacaaat 3567

3568 gtgtactataagacttttctaacaatttctaacttttagcattgtgaacgagacataagtgttaagaagacataacaattat 3647

3648 aatggaagaagtttgtctccatttatattatataattaccactttatgtattatattaggtatgtaaggagacataaca 3727

3728 attataaagagagaagtttgtatccatttatattatataactaccactttatattatacttatccacttatttaagt 3807

3808 tctttataagggtttgatccatgatatttctaataatttttagttgatatgtatatgaaagggtactatttgaactctcttac 3887

3888 tctgtataaagggttgatcatccttaaagtgggtctattttaattttattgtcttcttacagataaaaaaaaaattatgagt 3967

3968 tggtttgataaaatattgaaggattttaaataataataataataataataacatataatatatgtatataaattttattata 4047

4048 atataacattttatctataaaaaagtaaattattgtcataaatctatacaatcgtttagccttgctggacgactctcaatta 4127

4128 tttaaacgagagtaaacatatttgacttttttggttattttaacaaattattatttaacactatatgaaattttttttttt 4207

4208 atcggcaaggaaataaaattaaattaggaggagacaatggtgtgtcccaatccttatacaaccaacttccacaggaaggtc 4287

FIGURE 16 (CONT'D)

FIGURE 16 (CONT'D)

4288 aggtcggggacaacaaaaaacaggcaagggaaatTTTTTaatttgggtgtcttgtttgtgcataatttatgcagtaa 4367
4368 aacactacacataacccttttagcagtagagcaatggttgacctgtgcttagcttcttttattttattttttatcagc 4447
4448 aaagaataaataaaataaaatgagacacttcagggatgtttcaacccttatacaaaaccccaaaaacaagtttcctagca 4527
4528 ccctaccaactaaggtacc 4546
KpnI

034547-0106

FIGURE 17

PstI

1 ctgcaggaattcattgtactcccagtatcattatagtgaaagtttggctctctcgccggtgggtttttacctctattta 80

81 aaggggttttccacctaaaaattctgggtatcattctcactttacttggtactttaatttctcataatctttgggtgaaat 160

161 tatcacgcttccgcacacgatatccctacaaatttattatttggtaaacattttcaaaccgcataaaattttatgaagtc 240

241 ccgtctatctttaatgtagtctaacattttcatattgaaatatataatttacttaatttttagcgttggtagaaagcataa 320

321 tgattttattcttattcttcttcatataaatgtttaatatataataaacaattctttaccttaagaaggatttcccat 400

401 tttatattttaaaaaatatatttatcaaataatttttcaaccacgtaaatctcataataataagttgtttcaaaagtaataa 480

481 aatttaactccataaatttttttattcgactgatcttaaagcaacaccagtgacacaactagccattttttctttgaat 560

561 aaaaaaatccaattatcattgtatttttttatacaatgaaaatttcaccaaaccaatcatttgggtatttctgaagcaa 640

641 gtcattgttatgcaaaattctataattcccatttgacactacggaagtaactgaagatctgcttttacatgcgagacacat 720

721 cttctaaagtaattttaataatagttactatattcaagatttcatatatcaaatactcaatattacttctaaaaaattaa 800

801 ttagatataattaaaaatattacttttttaattttaagtttaattgttgaaatttgtagactattgatttatttctactat 880

881 gtttaaatgttttatagatagtttaaagtaaatataagtaatgtagtagagtgtagaggttacctaaccataaac 960

961 tataagatttatggtggactaattttcatatatttcttattgctttttaccttttcttggtatgtaagtccgtaactggaa 1040

1041 ttactgtgggttgccatggcactctgtggtcttttgggttcattgcatggatgcttgcgcaagaaaaagacaaagaacaaag 1120

1121 aaaaaagacaaaacagagagacaaaacgcaatcacacaaccaactcaaattagtcactggctgatcaagatcgccgctc 1200

1201 catgtatgtctaaatgccatgcaaagcaacacgtgcttaacatgcacttttaaatggctcacccatctcaaccacacaca 1280

1281 aacacattgccttttttctcatcatcaccacaaccacctgtatatattcattctcttccgccacctcaatttcttcaactt 1360

1361 caacacacgtcaacctgcattatgcgtgtcatcccatgccaaatctccatgcatttccaaccaccttctctcttatata 1440

1441 atacctataaatacctctaataatcactcacttctttcatcatccatccatccagagtactactactctactactataata 1520

1521 ccccaaccaactcatattcaataactactctact ATG AAT GGT CTC GAA ACT CAC AAC ACA AGG CTC 1587

1 M N G L E T H N T R L 11

1588 TGT ATC GTA GGA AGT GGC CCA GCG GCA CAC ACG GCG GCG ATT TAC GCA GCT AGG GCT GAA 1647

12 C I V G S G P A A H T A A I Y A A R A E 31

1648 CTT AAA CCT CTT CTC TTC GAA GGA TGG ATG GCT AAC GAC ATC GCT CCC GGT GGT CAA CTA 1707

32 L K P L L F E G W M A N D I A P G G Q L 51

1708 ACA ACC ACC ACC GAC GTC GAG AAT TTC CCC GGA TTT CCA GAA GGT ATT CTC GGA GTA GAG 1767

52 T T T T D V E N F P G F P E G I L G V E 71

FIGURE 17 (CONT'D)

1768 CTC ACT GAC AAA TTC CGT AAA CAA TCG GAG CGA TTC GGT ACT ACG ATA TTT ACA GAG ACG 1827
72 L T D K F R K Q S E R F G T T I F T E T 91

1828 GTG ACG AAA GTC GAT TTC TCT TCG AAA CCG TTT AAG CTA TTC ACA GAT TCA AAA GCC ATT 1887
92 V T K V D F S S K P F K L F T D S K A I 111

1888 CTC GCT GAC GCT GTG ATT CTC GCT ACT GGA GCT GTG GCT AAG CGG CTT AGC TTC GTT GGA 1947
112 L A D A V I L A T G A V A K R L S F V G 131

1948 TCT GGT GAA GGT TCT GGA GGT TTC TGG AAC CGT GGA ATC TCC GCT TGT GCT GTT TGC GAC 2007
132 S G E G S G G F W N R G I S A C A V C D 151

2008 GGA GCT GCT CCG ATA TTC CGT AAC AAA CCT CTT GCG GTG ATC GGT GGA GGC GAT TCA GCA 2067
152 G A A P I F R N K P L A V I G G G D S A 171

2068 ATG GAA GAA GCA AAC TTT CTT ACA AAA TAT GGA TCT AAA GTG TAT ATA ATC CAT AGG AGA 2127
172 M E E A N F L T K Y G S K V Y I I H R R 191

2128 GAT GCT TTT AGA GCG TCT AAG ATT ATG CAG CAG CGA GCT TTG TCT AAT CCT AAG ATT GAT 2187
192 D A F R A S K I M Q Q R A L S N P K I D 211

2188 GTG ATT TGG AAC TCG TCT GTT GTG GAA GCT TAT GGA GAT GGA GAA AGA GAT GTG CTT GGA 2247
212 V I W N S S V V E A Y G D G E R D V L G 231

2248 GGA TTG AAA GTG AAG AAT GTG GTT ACC GGA GAT GTT TCT GAT TTA AAA GTT TCT GGA TTG 2307
232 G L K V K N V V T G D V S D L K V S G L 251

2308 TTC TTT GCT ATT GGT CAT GAG CCA GCT ACC AAG TTT TTG GAT GGT GGT GTT GAG TTA GAT 2367
252 F F A I G H E P A T K F L D G G V E L D 271

2368 TCG GAT GGT TAT GTT GTC ACG AAG CCT GGT ACT ACA CAG ACT AGC GTT CCC GGA GTT TTC 2427
272 S D G Y V V T K P G T T Q T S V P G V F 291

2428 GCT GCG GGT GAT GTT CAG GAT AAG AAG TAT AGG CAA GCC ATC ACT GCT GCA GGA ACT GGG 2487
292 A A G D V Q D K K Y R Q A I T A A G T G 311

2488 TGC ATG GCA GCT TTG GAT GCA GAG CAT TAC TTA CAA GAG ATT GGA TCT CAG CAA GGT AAG 2547
312 C M A A L D A E H Y L Q E I G S Q Q G K 331

2548 AGT GAT ATG GCG GAT ACA GCT AGA GGA ACC CAT CAC GAT ATC ATC GGC AGA GAC CAG TAC 2607
332 S D M A D T A R G T H H D I I G R D Q Y 351

2608 CCG ATG ATG GGC CGA GAC CGA GAC CAG TAC CAG ATG TCC GGA CGA GGA TCT GAC TAC TCC 2667
352 P M M G R D R D Q Y Q M S G R G S D Y S 371

2668 AAG TCT AGG CAG ATT GCT AAA GCT GCA ACT GCT GTC ACA GCT GGT GGT TCC CTC CTT GTT 2727
372 K S R Q I A K A A T A V T A G G S L L V 391

FIGURE 17 (CONT'D)

FIGURE 17 (CONT'D)

2728 CTC TCC AGC CTT ACC CTT GTT GGA ACT GTC ATA GCT TTG ACT GTT GCA ACA CCT CTG CTC 2787
392 L S S L T L V G T V I A L T V A T P L L 411

2788 GTT ATC TTC AGC CCA ATC CTT GTC CCG GCT CTC ATC ACA GTT GCA CTC CTC ATC ACC GGT 2847
412 V I F S P I L V P A L I T V A L L I T G 431

2848 TTT CTT TCC TCT GGA GGG TTT GGC ATT GCC GCT ATA ACC GTT TTC TCT TGG ATT TAC AA g 2907
432 F L S S G G F G I A A I T V F S W I Y K 451

2908 taagcacacatttatcatcttacttcataattttgtgcaatatgtgcatgcatgtgttgagccagtagctttggatcaat 2987

2988 ttttttggtcgaataacaaatgtaacaataagaaattgcaaattcttagggaacatttgggttaactaaatacgaatttga 3067

3068 cctagctagcttgaatgtgtctgtgtatatcatctatataggtaaaatgcttggatgatacctattgattgtgaatag 3146

3147 G TAC GCA ACG GGA GAG CAC CCA CAG GGA TCA GAC AAG TTG GAC AGT GCA AGG ATG AAG 3204
452 Y A T G E H P Q G S D K L D S A R M K 470

3205 TTG GGA AGC AAA GCT CAG GAT CTG AAA GAC AGA GCT CAG TAC TAC GGA CAG CAA CAT ACT 3264
471 L G S K A Q D L K D R A Q Y Y G Q Q H T 490

3265 GGT GGG GAA CAT GAC CGT GAC CGT ACT CGT GGT GGC CAG CAC ACT ACT TAA gcttaataagta 3327
491 G G E H D R D R T R G G Q H T T * HindIII 507

3328 tgaactaaaatgcatgtaggtgtgaagagctcatggagagcatggaatattgtatccgaccatgtaacagtataataactg 3407

3408 agctccatctcacttcttctatgaataaacaaggatgttatgatataattaacactctatctatgcaccttattgttcta 3487

3488 tgataaatttctcttattattataaatcatctgaatcgtagcggttatggaatgcttcaaatagtacaaaaacaaatg 3567

3568 tgtactataagacttttctaacaatttctaacttttagcattgtgaacgagacataagtggttaagaagacataacaattata 3647

3648 atggaagaagtttgtctccatttatattatataactaccacttatgtattatattaggatgttaaggagacataacaa 3727

3728 ttataaagagagaagtttgtatccatttatattatataactaccactttatatattatacttatccacttatttaattgt 3807

3808 ctttataagggttgatccatgatatttctaataatttttagttgatatgtatatgaaagggtactatttgaactctcttact 3887

3888 ctgtataaagggttgatccatccttaaagtgggtctatttaattttattgcttcttacagataaaaaaaaaattatgagtt 3967

3968 gggttgataaaatattgaaggatttaaaataataataataataataacatataatatgtatataaatttattataa 4047

4048 tataacatttatctataaaaaagtaaatattgtcataaatctatacaatcgtttagccttgctggacgactctcaattat 4127

4128 ttaaacgagagtaaacatatttgactttttggttatttaacaaattattatttaacactatatgaaattttttttttta 4207

4208 tcggcaaggaaataaaattaaattaggagggacaatggtgtgtcccaatccttataacaaccaacttccacaggaaggtca 4287

FIGURE 17 (CONT'D)

FIGURE 18

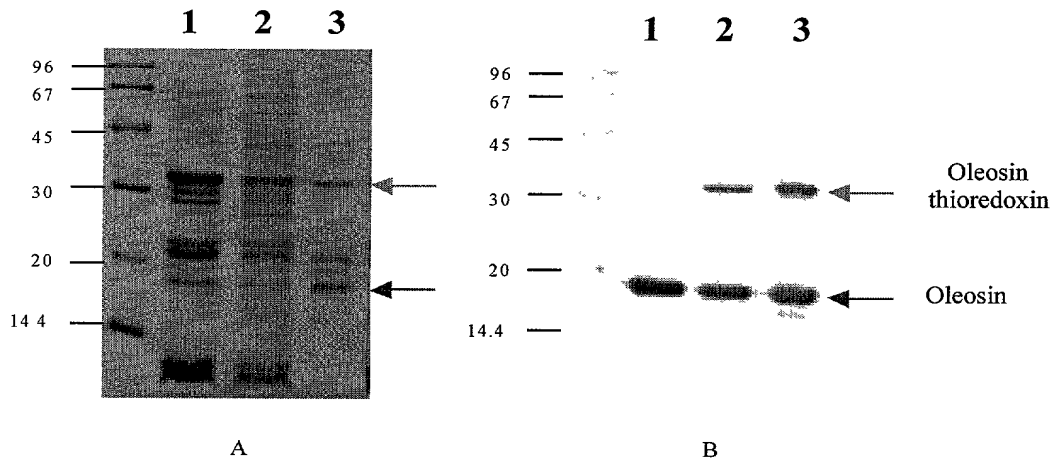
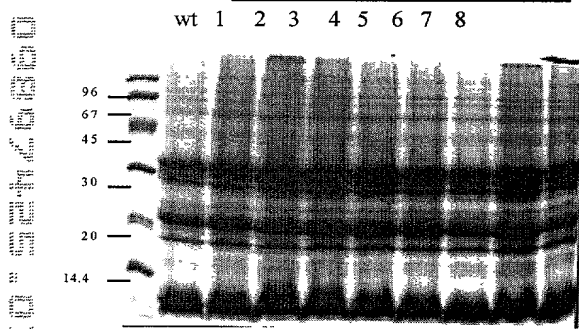


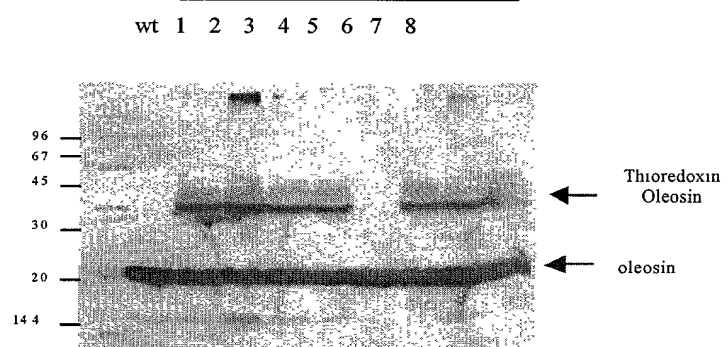
FIGURE 19

PSBS2521 transformants



A

PSBS2521 transformants



B

FIGURE 20

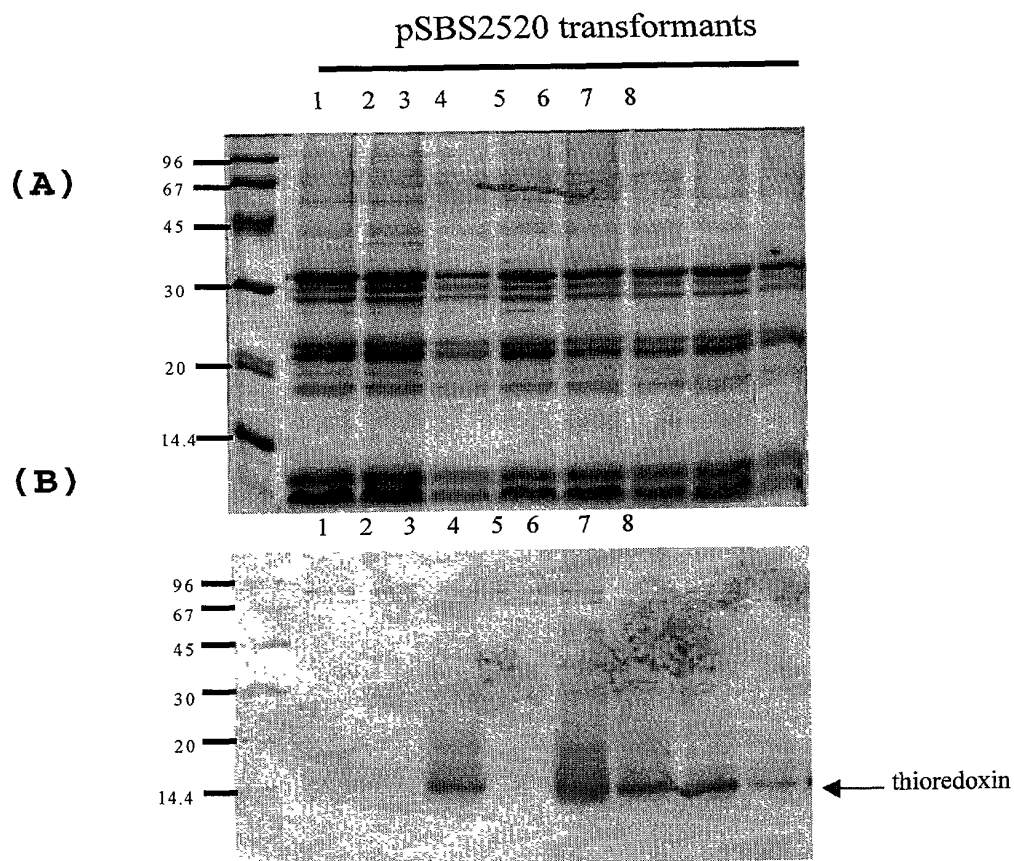


FIGURE 21

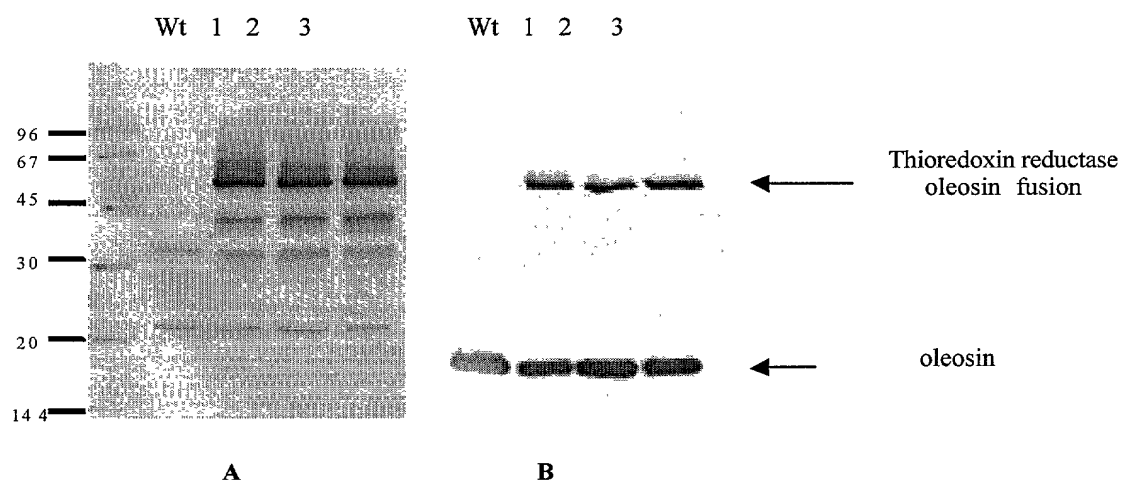


FIGURE 22

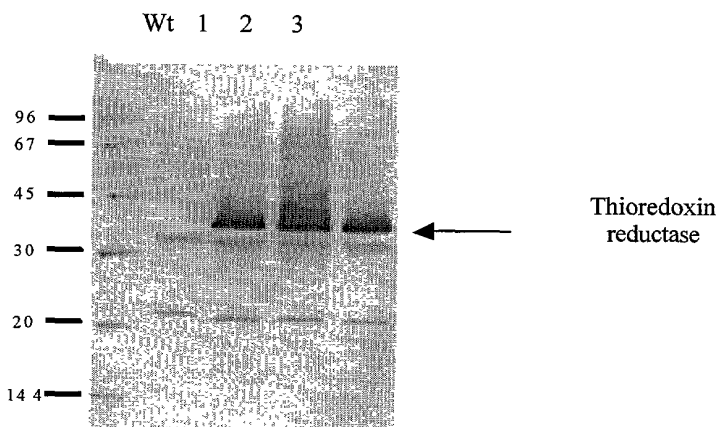


FIGURE 23

